

T640X

SEQUENCE LISTING

07257/017002

(1) GENERAL INFORMATION:

(i) APPLICANT: KARIN, MICHAEL
HIBI, MASAHIKO
LIN, ANNING

(ii) TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: La Jolla
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 92037

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/444,393
(B) FILING DATE: 19-MAY-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Haile, Ph.D., Lisa A.,
(B) REGISTRATION NUMBER: 38,347
(C) REFERENCE/DOCKET NUMBER: 07257/017002

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

64

(vii) IMMEDIATE SOURCE:

(B) CLONE: c-Jun/JNK binding site

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..47

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ile Leu Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser
1 5 10 15

Leu Lys Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro
20 25 30

Asp Val Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: N-terminal primer

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCTGCAGGAT CCCCATGACT GCAAAGATGG AAACG

35

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

63

(B) CLONE: N-terminal primer

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCTGCAGGAT CCCCAGACGAT GCCCTCAACG CCTC

34

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: N-terminal primer

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCTGCAGGAT CCCCAGAGAGC GGACCTTATG GCTAC

35

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: N-terminal primer

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..35

66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCTGCAGGAT CCCC GCCGAC CCAGTGGGGA GCCTG

35

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: N-terminal primer

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCTGCAGGAT CCCCAAGAAC TCGGACCTCC TCACC

35

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: C-terminal primer

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGAATTCTGC AGGCGCTCCA GCTCGGGCGA

30

67

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: C-terminal primer

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGAATTCCTG CAGGTCGGCG TGGTGGTGAT GTG

33

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2099 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Jun

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 414..1406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCCGGG GCGGCCAAGA CCCGCCGCCG GCCGGCCACT GCAGGGTCCG CACTGATCCG 60
CTCCGGCGGA GAGCCGCTGC TCTGGGAAGT GAGTTCGCCT GCGGACTCCG AGGAACCGCT 120
GCGCACGAAG AGCGCTCACT GAGTGACCGC GACTTTTCAA AGCCGGGTAG CGCGCGCGAG 180
TCGACAAGTA AGAGTGCGGG AGGCATCTTA ATTAACCCTG CGCTCCCTGG AGCGAGCTGG 240
TGAGGAGGGC GCAGCGGGGA CGACAGCCAG CGGGTGCGTG CGCTCTTAGA GAAACTTTCC 300

CTGTCAAAGG CTCCGGGGGG CGCGGGTGTC CCCCCTTGC CAGAGCCCTG TTGCGGCCCC 360

GAAACTTGTG CGCGCACGCC AAATAACCT CACGTGAAGT GACGGACTGT TCT ATG 416
Met
1

ACT GCA AAG ATG GAA ACG ACC TTC TAT GAC GAT GCC CTC AAC GCC TCG 464
Thr Ala Lys Met Glu Thr Thr Phe Tyr Asp Asp Ala Leu Asn Ala Ser
5 10 15

TTC CTC CCG TCC GAG AGC GGA CCT TAT GGC TAC AGT AAC CCC AAG ATC 512
Phe Leu Pro Ser Glu Ser Gly Pro Tyr Gly Tyr Ser Asn Pro Lys Ile
20 25 30

CTG AAA CAG AGC ATG ACC CTG AAC CTG GCC GAC CCA GTG GGG AGC CTG 560
Leu Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser Leu
35 40 45

AAG CCG CAC CTC CGC GCC AAG AAC TCG GAC CTC CTC ACC TCG CCC GAC 608
Lys Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro Asp
50 55 60 65

GTG GGG CTG CTC AAG CTG GCG TCG CCC GAG CTG GAG CGC CTG ATA ATC 656
Val Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu Ile Ile
70 75 80

CAG TCC AGC AAC GGG CAC ATC ACC ACC ACG CCG ACC CCC ACC CAG TTC 704
Gln Ser Ser Asn Gly His Ile Thr Thr Thr Pro Thr Pro Thr Gln Phe
85 90 95

CTG TGC CCC AAG AAC GTG ACA GAT GAG CAG GAG GGG TTC GCC GAG GGC 752
Leu Cys Pro Lys Asn Val Thr Asp Glu Gln Glu Gly Phe Ala Glu Gly
100 105 110

TTC GTG CGC GCC CTG GCC GAA CTG CAC AGC CAG AAC ACG CTG CCC AGC 800
Phe Val Arg Ala Leu Ala Glu Leu His Ser Gln Asn Thr Leu Pro Ser
115 120 125

GTC ACG TCG GCG GCG CAG CCG GTC AAC GGG GCA GGC ATG GTG GCT CCC 848
Val Thr Ser Ala Ala Gln Pro Val Asn Gly Ala Gly Met Val Ala Pro
130 135 140 145

GCG GTA GCC TCG GTG GCA GGG GGC AGC GGC AGC GGC GGC TTC AGC GCC 896
Ala Val Ala Ser Val Ala Gly Gly Ser Gly Ser Gly Gly Phe Ser Ala
150 155 160

AGC CTG CAC AGC GAG CCG CCG GTC TAC GCA AAC CTC AGC AAC TTC AAC 944
Ser Leu His Ser Glu Pro Pro Val Tyr Ala Asn Leu Ser Asn Phe Asn
165 170 175

CCA GGC GCG CTG AGC AGC GGC GGC GGG GCG CCC TCC TAC GGC GCG GCC 992
Pro Gly Ala Leu Ser Ser Gly Gly Gly Ala Pro Ser Tyr Gly Ala Ala
180 185 190

GGC CTG GCC TTT CCC GCG CAA CCC CAG CAG CAG CAG CAG CCG CCG CAC 1040
 Gly Leu Ala Phe Pro Ala Gln Pro Gln Gln Gln Gln Gln Pro Pro His
 195 200 205

CAC CTG CCC CAG CAG ATG CCC GTG CAG CAC CCG CGG CTG CAG GCC CTG 1088
 His Leu Pro Gln Gln Met Pro Val Gln His Pro Arg Leu Gln Ala Leu
 210 215 220 225

AAG GAG GAG CCT CAG ACA GTG CCC GAG ATG CCC GGC GAG ACA CCG CCC 1136
 Lys Glu Glu Pro Gln Thr Val Pro Glu Met Pro Gly Glu Thr Pro Pro
 230 235 240

CTG TCC CCC ATC GAC ATG GAG TCC CAG GAG CGG ATC AAG GCG GAG AGG 1184
 Leu Ser Pro Ile Asp Met Glu Ser Gln Glu Arg Ile Lys Ala Glu Arg
 245 250 255

AAG CGC ATG AGG AAC CGC ATC GCT GCC TCC AAG TGC CGA AAA AGG AAG 1232
 Lys Arg Met Arg Asn Arg Ile Ala Ala Ser Lys Cys Arg Lys Arg Lys
 260 265 270

CTG GAG AGA ATC GCC CGG CTG GAG GAA AAA GTG AAA ACC TTG AAA GCT 1280
 Leu Glu Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala
 275 280 285

CAG AAC TCG GAG CTG GCG TCC ACG GCC AAC ATG CTC AGG GAA CAG GTG 1328
 Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val
 290 295 300 305

GCA CAG CTT AAA CAG AAA GTC ATG AAC CAC GTT AAC AGT GGG TGC CAA 1376
 Ala Gln Leu Lys Gln Lys Val Met Asn His Val Asn Ser Gly Cys Gln
 310 315 320

CTC ATG CTA ACG CAG CAG TTG CAA ACA TTT TGAAGAGAGA CCGTCGGGGG 1426
 Leu Met Leu Thr Gln Gln Leu Gln Thr Phe
 325 330

CTGAGGGGGCA ACGAAGAAAA AAAATAACAC AGAGAGACAG ACTTGAGAAC TTGACAAGTT 1486

GCGACGGAGA GAAAAAAGAA GTGTCCGAGA ACTAAAGCCA AGGGTATCCA AGTTGGACTG 1546

GGTTCGGTCT GACGGCGCCC CCA GTGTGCA CGAGTGGGAA GGACTTGGTC GCGCCCTCCC 1606

TTGGCGTGGA GCCAGGGAGC GGCCGCCTGC GGGCTGCCCC GCTTTGCGGA CGGGCTGTCC 1666

CCGCGCGAAC GGAACGTTGG ACTTTCGTTA ACATTGACCA AGAACTGCAT GGACCTAACA 1726

TTCGATCTCA TTCAGTATTA AAGGGGGGAG GGGGAGGGGG TTACAAACTG CAATAGAGAC 1786

TGTAGATTGC TTCTGTAGTA CTCCTTAAGA ACACAAAGCG GGGGAGGGGT TGGGGAGGGG 1846

CGGCAGGAGG GAGGTTTGTG AGAGCGAGGC TGAGCCTACA GATGAACTCT TTCTGGCCTG 1906

CTTTCGTTAA CTGTGTATGT ACATATATAT ATTTTAAAT TTGATTAAAG CTGATTACTG 1966

TCAATAAACA GCTTCATGCC TTTGTAAGTT ATTTCTTGTT TGTTCGTTTG GGTATCCTGC 2026
 CCAGTGTGTG TTGTAAATAA GAGATTGGA GCACTCTGAG TTTACCATTT GTAATAAAGT 2086
 ATATAATTTT TTT 2099

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Thr Ala Lys Met Glu Thr Thr Phe Tyr Asp Asp Ala Leu Asn Ala
 1 5 10 15
 Ser Phe Leu Pro Ser Glu Ser Gly Pro Tyr Gly Tyr Ser Asn Pro Lys
 20 25 30
 Ile Leu Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser
 35 40 45
 Leu Lys Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro
 50 55 60
 Asp Val Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu Ile
 65 70 75 80
 Ile Gln Ser Ser Asn Gly His Ile Thr Thr Thr Pro Thr Pro Thr Gln
 85 90 95
 Phe Leu Cys Pro Lys Asn Val Thr Asp Glu Gln Glu Gly Phe Ala Glu
 100 105 110
 Gly Phe Val Arg Ala Leu Ala Glu Leu His Ser Gln Asn Thr Leu Pro
 115 120 125
 Ser Val Thr Ser Ala Ala Gln Pro Val Asn Gly Ala Gly Met Val Ala
 130 135 140
 Pro Ala Val Ala Ser Val Ala Gly Gly Ser Gly Ser Gly Gly Phe Ser
 145 150 155 160
 Ala Ser Leu His Ser Glu Pro Pro Val Tyr Ala Asn Leu Ser Asn Phe
 165 170 175
 Asn Pro Gly Ala Leu Ser Ser Gly Gly Gly Ala Pro Ser Tyr Gly Ala
 180 185 190

Ala Gly Leu Ala Phe Pro Ala Gln Pro Gln Gln Gln Gln Gln Pro Pro
195 200 205

His His Leu Pro Gln Gln Met Pro Val Gln His Pro Arg Leu Gln Ala
210 215 220

Leu Lys Glu Glu Pro Gln Thr Val Pro Glu Met Pro Gly Glu Thr Pro
225 230 235 240

Pro Leu Ser Pro Ile Asp Met Glu Ser Gln Glu Arg Ile Lys Ala Glu
245 250 255

Arg Lys Arg Met Arg Asn Arg Ile Ala Ala Ser Lys Cys Arg Lys Arg
260 265 270

Lys Leu Glu Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys
275 280 285

Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln
290 295 300

Val Ala Gln Leu Lys Gln Lys Val Met Asn His Val Asn Ser Gly Cys
305 310 315 320

Gln Leu Met Leu Thr Gln Gln Leu Gln Thr Phe
325 330